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RAW SEQUENCE LISTING DATE: 12/13/2001  
PATENT APPLICATION: US/09/854,356 TIME: 15:02:09

Input Set : N:\paola\09854356.txt  
Output Set: N:\CRF3\12132001\I854356.raw

3 <110> APPLICANT: Cheever, Martin A.  
4 Gheysen, Dirk  
5 Corixa Corporation  
6 SmithKline Beecham Biologicals S. A.  
8 <120> TITLE OF INVENTION: HER-2/neu Fusion Proteins  
10 <130> FILE REFERENCE: 014058-009810PC  
12 <140> CURRENT APPLICATION NUMBER: 09/854,356  
13 <141> CURRENT FILING DATE: 2001-05-09  
15 <150> PRIOR APPLICATION NUMBER: 09/493,480  
16 <151> PRIOR FILING DATE: 2000-01-28  
18 <160> NUMBER OF SEQ ID NOS: 26  
20 <170> SOFTWARE: PatentIn Ver. 2.1  
22 <210> SEQ ID NO: 1  
23 <211> LENGTH: 1255  
24 <212> TYPE: PRT  
25 <213> ORGANISM: Homo sapiens  
27 <220> FEATURE:  
28 <223> OTHER INFORMATION: human HER-2/neu protein  
30 <220> FEATURE:  
31 <221> NAME/KEY: DOMAIN  
32 <222> LOCATION: (1)..(653)  
33 <223> OTHER INFORMATION: extracellular domain (ECD)  
35 <220> FEATURE:  
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37 <222> LOCATION: (676)..(1255)  
38 <223> OTHER INFORMATION: intracellular domain (ICD)  
40 <220> FEATURE:  
41 <221> NAME/KEY: DOMAIN  
42 <222> LOCATION: (990)..(1255)  
43 <223> OTHER INFORMATION: phosphorylation domain (PD)  
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46 <221> NAME/KEY: DOMAIN  
47 <222> LOCATION: (990)..(1048)  
48 <223> OTHER INFORMATION: fragment of the phosphorylation domain, preferred  
49 portion (delta PD)  
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53 1 5 10 15  
55 Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys  
56 20 25 30  
58 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His  
59 35 40 45  
61 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr  
62 50 55 60  
64 Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val  
65 65 70 75 80  
67 Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu

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68	85	90	95
70	Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr		
71	100	105	110
73	Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro		
74	115	120	125
76	Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser		
77	130	135	140
79	Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln		
80	145	150	155
82	160		
83	Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn		
85	165	170	175
86	Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys		
88	180	185	190
89	His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser		
91	195	200	205
92	Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys		
94	210	215	220
95	Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys		
97	225	230	235
98	240		
99	Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu		
100	245	250	255
101	His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val		
103	260	265	270
104	Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg		
106	275	280	285
107	Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu		
109	290	295	300
110	Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln		
112	305	310	315
113	320	330	335
115	325		
116	Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu		
118	340	345	350
119	Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys		
121	355	360	365
122	Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp		
124	370	375	380
125	Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe		
127	385	390	395
128	Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro		
130	405	410	415
131	Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg		
133	420	425	430
134	Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu		
136	435	440	445
137	Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly		
139	450	455	460
140	Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val		
	465	470	475
			480

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142 Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr  
143 485 490 495  
145 Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His  
146 500 505 510  
148 Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys  
149 515 520 525  
151 Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys  
152 530 535 540  
154 Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys  
155 545 550 555 560  
157 Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys  
158 565 570 575  
160 Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp  
161 580 585 590  
163 Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu  
164 595 600 605  
166 Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln  
167 610 615 620  
169 Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys  
170 625 630 635 640  
172 Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser  
173 645 650 655  
175 Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly  
176 660 665 670  
178 Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg  
179 675 680 685  
181 Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly  
182 690 695 700  
184 Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu  
185 705 710 715 720  
187 Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys  
188 725 730 735  
190 Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile  
191 740 745 750  
193 Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu  
194 755 760 765  
196 Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg  
197 770 775 780  
199 Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu  
200 785 790 795 800  
202 Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg  
203 805 810 815  
205 Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly  
206 820 825 830  
208 Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala  
209 835 840 845  
211 Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe  
212 850 855 860  
214 Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp

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215	865	870	875	880												
217	Gly	Gly	Lys	Val	Pro	Ile	Lys	Trp	Met	Ala	Leu	Glu	Ser	Ile	Leu	Arg
218					885				890						895	
220	Arg	Arg	Phe	Thr	His	Gln	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr	Val
221						900				905					910	
223	Trp	Glu	Leu	Met	Thr	Phe	Gly	Ala	Lys	Pro	Tyr	Asp	Gly	Ile	Pro	Ala
224						915			920					925		
226	Arg	Glu	Ile	Pro	Asp	Leu	Leu	Glu	Lys	Gly	Glu	Arg	Leu	Pro	Gln	Pro
227						930			935					940		
229	Pro	Ile	Cys	Thr	Ile	Asp	Val	Tyr	Met	Ile	Met	Val	Lys	Cys	Trp	Met
230						945			950			955			960	
232	Ile	Asp	Ser	Glu	Cys	Arg	Pro	Arg	Phe	Arg	Glu	Leu	Val	Ser	Glu	Phe
233						965				970					975	
235	Ser	Arg	Met	Ala	Arg	Asp	Pro	Gln	Arg	Phe	Val	Val	Ile	Gln	Asn	Glu
236						980			985					990		
238	Asp	Leu	Gly	Pro	Ala	Ser	Pro	Leu	Asp	Ser	Thr	Phe	Tyr	Arg	Ser	Leu
239						995			1000					1005		
241	Leu	Glu	Asp	Asp	Asp	Met	Gly	Asp	Leu	Val	Asp	Ala	Glu	Glu	Tyr	Leu
242						1010			1015					1020		
244	Val	Pro	Gln	Gln	Gly	Phe	Phe	Cys	Pro	Asp	Pro	Ala	Pro	Gly	Ala	Gly
245						1025			1030			1035			1040	
247	Gly	Met	Val	His	His	Arg	His	Arg	Ser	Ser	Ser	Thr	Arg	Ser	Gly	Gly
248						1045				1050				1055		
250	Gly	Asp	Leu	Thr	Leu	Gly	Leu	Glu	Pro	Ser	Glu	Glu	Glu	Ala	Pro	Arg
251						1060			1065					1070		
253	Ser	Pro	Leu	Ala	Pro	Ser	Glu	Gly	Ala	Gly	Ser	Asp	Val	Phe	Asp	Gly
254						1075			1080					1085		
256	Asp	Leu	Gly	Met	Gly	Ala	Ala	Lys	Gly	Leu	Gln	Ser	Leu	Pro	Thr	His
257						1090			1095					1100		
259	Asp	Pro	Ser	Pro	Leu	Gln	Arg	Tyr	Ser	Glu	Asp	Pro	Thr	Val	Pro	Leu
260						1105			1110			1115			1120	
262	Pro	Ser	Glu	Thr	Asp	Gly	Tyr	Val	Ala	Pro	Leu	Thr	Cys	Ser	Pro	Gln
263						1125				1130				1135		
265	Pro	Glu	Tyr	Val	Asn	Gln	Pro	Asp	Val	Arg	Pro	Gln	Pro	Pro	Ser	Pro
266						1140			1145					1150		
268	Arg	Glu	Gly	Pro	Leu	Pro	Ala	Ala	Arg	Pro	Ala	Gly	Ala	Thr	Leu	Glu
269						1155			1160					1165		
271	Arg	Pro	Lys	Thr	Leu	Ser	Pro	Gly	Lys	Asn	Gly	Val	Val	Lys	Asp	Val
272						1170			1175					1180		
274	Phe	Ala	Phe	Gly	Gly	Ala	Val	Glu	Asn	Pro	Glu	Tyr	Leu	Thr	Pro	Gln
275						1185			1190			1195			1200	
277	Gly	Gly	Ala	Ala	Pro	Gln	Pro	His	Pro	Pro	Pro	Ala	Phe	Ser	Pro	Ala
278						1205				1210				1215		
280	Phe	Asp	Asn	Leu	Tyr	Tyr	Trp	Asp	Gln	Asp	Pro	Pro	Glu	Arg	Gly	Ala
281						1220			1225					1230		
283	Pro	Pro	Ser	Thr	Phe	Lys	Gly	Thr	Pro	Thr	Ala	Glu	Asn	Pro	Glu	Tyr
284						1235			1240					1245		
286	Leu	Gly	Leu	Asp	Val	Pro	Val									
287						1250			1255							

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290 <210> SEQ ID NO: 2  
291 <211> LENGTH: 1256  
292 <212> TYPE: PRT  
293 <213> ORGANISM: Rattus sp.  
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296 <223> OTHER INFORMATION: rat HER-2/neu protein  
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299 <221> NAME/KEY: DOMAIN  
300 <222> LOCATION: (1)..(654)  
301 <223> OTHER INFORMATION: extracellular domain (ECD)  
303 <220> FEATURE:  
304 <221> NAME/KEY: DOMAIN  
305 <222> LOCATION: (677)..(1256)  
306 <223> OTHER INFORMATION: intracellular domain (ICD)  
308 <220> FEATURE:  
309 <221> NAME/KEY: DOMAIN  
310 <222> LOCATION: (721)..(998)  
311 <223> OTHER INFORMATION: kinase domain (KD)  
313 <220> FEATURE:  
314 <221> NAME/KEY: DOMAIN  
315 <222> LOCATION: (991)..(1256)  
316 <223> OTHER INFORMATION: phosphorylation domain (PD)  
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320 <222> LOCATION: (991)..(1049)  
321 <223> OTHER INFORMATION: fragment of the phosphorylation domain, preferred  
322 portion (delta PD)  
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325 Met Glu Leu Ala Ala Trp Cys Arg Trp Gly Phe Leu Leu Ala Leu Leu  
326 1 5 10 15  
328 Pro Pro Gly Ile Ala Gly Thr Gln Val Cys Thr Gly Thr Asp Met Lys  
329 20 25 30  
331 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His  
332 35 40 45  
334 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr  
335 50 55 60  
337 Val Pro Ala Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val  
338 65 70 75 80  
340 Gln Gly Tyr Met Leu Ile Ala His Asn Gln Val Lys Arg Val Pro Leu  
341 85 90 95  
343 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Lys Tyr  
344 100 105 110  
346 Ala Leu Ala Val Leu Asp Asn Arg Asp Pro Gln Asp Asn Val Ala Ala  
347 115 120 125  
349 Ser Thr Pro Gly Arg Thr Pro Glu Gly Leu Arg Glu Leu Gln Leu Arg  
350 130 135 140  
352 Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Arg Gly Asn Pro  
353 145 150 155 160  
355 Gln Leu Cys Tyr Gln Asp Met Val Leu Trp Lys Asp Val Phe Arg Lys

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